



SEQUENCE LISTING

Watson, Dennis K. Papas, Takis S. (Deceased) Papas, Tula C. (Legal Representative)

<120> Methods and compositions for the diagnosis and treatment of cancer based on transcription factor ETS2 10545-015-999 <130> <140> 09/841,963 <141> 2001-04-25 PCT/US99/27805 <150> <151> 1999-11-23 06/109,850 <150> <151> 1998-11-25 <160> <170> PatentIn version 3.0 <210> 1 <211> 1894 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (416)..(1423)<400> 1 gtotgactto otoccagoac attootgoac totgoogtgt ocacactgoo coacagacco 60 agtectecaa geetgetgee ageteeetge aageeeetea ggttgggeet tgeeaeggtg 120 ccagcaggca gccctgggct gggggtaggg gactccctac aggcacgcag ccctgagacc 180 gccaccagcc accepttgag ggtggccagg cccccagtgg ccaacctgag tgctgcctct 240 gecaccagec etgetggeec etggtteege tggeececca gatgeetgge tgagaeaege 300 360 cagtggcctc agctgcccac acctcttccc ggcccctgga gttggcactg cagcagacag 418 ctccctgggc accaggcagc taacagacac agccgccagc ccaaacagca gcggc atg Met 466 ggc agc gcc agc ccg ggt ctg agc agc gta tcc ccc agc cac ctc ctg Gly Ser Ala Ser Pro Gly Leu Ser Ser Val Ser Pro Ser His Leu Leu 10 ctg ccc ccc gac acg gtg tcg cgg aca ggc ttg gag aag gcg gca gcg 514 Leu Pro Pro Asp Thr Val Ser Arg Thr Gly Leu Glu Lys Ala Ala Ala 25 20 30 562 ggg gca gtg ggt ctc gag aga cgg gac tgg agt ccc agt cca ccc gcc Gly Ala Val Gly Leu Glu Arg Arg Asp Trp Ser Pro Ser Pro Pro Ala 40 45 acg ccc gag cag ggc ctg tcc gcc ttc gac ctc tcc tac ttt gac atg 610 Thr Pro Glu Gln Gly Leu Ser Ala Phe Asp Leu Ser Tyr Phe Asp Met 55 60 658 ctg tac cct gag gac agc tgg gca gcc aag gcc cct ggg gcc agc Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala Ser 706 agt cgg gag gag cca cct gac cag cct gag cag tgc ccg gtc att gac

Ser Arg Glu Glu Pro Pro Asp Gln Pro Glu Gln Cys Pro Val Ile Asp

85

```
agc caa gcc cca gcg ggc acc ctg gac ttg gtg ccc ggc ggg ctg acc
                                                                      754
Ser Gln Ala Pro Ala Gly Thr Leu Asp Leu Val Pro Gly Gly Leu Thr
                            105
                                                110
        100
ttg gag gag cac tcg ctg gag cag gtg cag tcc atg gtg gtg ggc gaa
                                                                      802
Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly Glu
                        120
                                                                      850
gtg ctc aag gac atc gag acg gcc tgc aag ctg ctc aac atc acc gca
Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr Ala
                                         140
                    135
130
gat ccc atg gac tgg agc ccc agc aat gtg cag aag tgg ctc ctg tgg
                                                                      898
Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu Trp
                150
                                    155
aca gag cac caa tac cgg ctg ccc ccc atg ggc aag gcc ttc cag gag
                                                                      946
Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln Glu
                                170
                                                     175
ctg gcg ggc aag gag ctg tgc gcc atg tcg gag gag cag ttc cgc cag
                                                                      994
Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg Gln
        180
                            185
                                                 190
                                                                     1042
cgc tcg ccc ctg ggt ggg gat gtg ctg cac gcc cac ctg gac atc tgg
Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile Trp
                        200
                                             205
    195
aag tca gcg gcc tgg atg aaa gag cgg act tca cct ggg gcg att cac
                                                                     1090
Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile His
210
                    215
                                         220
tac tgt gcc tcg acc agt gag gag agc tgg acc gac agc gag gtg gac
                                                                     1138
Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val Asp
                230
                                    235
tca tca tgc tcc ggg cag ccc atc cac ctg tgg cag ttc ctc aag gag
                                                                     1186
Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys Glu
                                250
                                                     255
                                                                     1234
ttg cta ctc aag ccc cac agc tat ggc cgc ttc att agg tgg ctc aac
Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu Asn
                            265
                                                 270
        260
                                                                     1282
aag gag aag ggc atc ttc aaa att gag gac tca gcc cag gtg gcc cgg
Lys Glu Lys Gly Ile Phe Lys Ile Glu Asp Ser Ala Gln Val Ala Arg
    275
                        280
                                             285
ctg tgg ggc atc cgc aag aac cgt ccc gcc atg aac tgc gac aag ctg
                                                                     1330
Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Cys Asp Lys Leu
                                                             305
                    295
                                         300
age ege tee ate ege eag tet tae aag aag gge ate ate egg aag eea
                                                                     1378
Ser Arg Ser Ile Arg Gln Ser Tyr Lys Lys Gly Ile Ile Arg Lys Pro
                310
gac atc tcc cag cgc ctc gtc tac cag ttc gtg cac ccc atc tga
                                                                     1423
Asp Ile Ser Gln Arg Leu Val Tyr Gln Phe Val His Pro Ile
            325
qtqcctqqcc caqqqcctqa aacccqccct caqqqqcctc tctcctqcct gccctgcctc
                                                                     1483
                                                                     1543
agccaggccc tgagatgggg gaaaacgggc agtgtgctct gctgctctga ccttccagag
cccaaggtca gggagggca accaactgcc ccagggggat atgggtcctc tggggccttc
                                                                     1603
gggaccatgg ggcaggggtg cttcctcctc aggcccagct gctcccctgg aggacagagg
gagacagggc tgctccccaa cacctgcctc tgaccccagc atttccagag cagagcctac
                                                                     1723
                                                                     1783
agaagggcag tgactcgaca aaggccacag gcagtccagg cctctctctg ctccatcccc
ctgcctccca ttctgcacca cacctggcat ggtgcaggga gacatctgca cccctcagtt
                                                                     1843
                                                                     1894
gggcagccag gagtgccccc gggaatggat aataaagata ctagagaact g
<210>
       2
       335
<211>
<212>
       PRT
<213>
       Homo sapiens
<400> 2
Met Gly Ser Ala Ser Pro Gly Leu Ser Ser Val Ser Pro Ser His Leu
                                     10
```

Leu Leu Pro Pro Asp Thr Val Ser Arg Thr Gly Leu Glu Lys Ala Ala 25 Ala Gly Ala Val Gly Leu Glu Arg Arg Asp Trp Ser Pro Ser Pro Pro Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Asp Leu Ser Tyr Phe Asp Met Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala 70 Ser Ser Arg Glu Glu Pro Pro Asp Gln Pro Glu Gln Cys Pro Val Ile Asp Ser Gln Ala Pro Ala Gly Thr Leu Asp Leu Val Pro Gly Gly Leu Thr Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly 120 Glu Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr Ala Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu Trp Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln 170 Glu Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg Gln Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile 200 Trp Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile His Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val Asp Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys 250 245 Glu Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu Asn Lys Glu Lys Gly Ile Phe Lys Ile Glu Asp Ser Ala Gln Val Ala Arg Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Cys Asp Lys Leu Ser Arg Ser Ile Arg Gln Ser Tyr Lys Lys Gly Ile Ile Arg Lys Pro Asp Ile Ser Gln Arg Leu Val Tyr Gln Phe Val His Pro Ile 330 <210> <211> 1704

```
<212>
      DNA
<213>
      Mus sp.
<220>
<221>
      CDS
      (362)..(1336)
<222>
<400> 3
tqtccgctct gcctcccaca cctagcaccc cagcccgctg ctgccccggt gagaaccccc
                                                                     60
agcttgggcc ttgtcatggt gccagcaggt ggccctgagc ttctgacagg ggcctgccta
                                                                    120
tagacctgca ggcctgaggc ctcagactca cactcaaggg gcaagaggcc ctggtggccc
acctaagage cacctetgte eccagecetg etgececaet gatgtetgae tgagacceag
                                                                    240
                                                                    300
cagtgaccct gagetgeetg eccaetgeet ecteetggte ectgaggttg getetgeega
qqacqqacqa ctcttctgaa gcaggcggct aacggaagca gccccaagcc tccaccgcag
                                                                    360
                                                                     409
c atg ggc agt gcc agc cca ggc ctg agc aac gtg tcc ccc ggt tgc ctg
 Met Gly Ser Ala Ser Pro Gly Leu Ser Asn Val Ser Pro Gly Cys Leu
                                     10
                                                                     457
Leu Leu Phe Pro Asp Val Ala Pro Arg Thr Gly Thr Glu Lys Ala Ala
                                25
            20
tca gga gca atg ggc cct gag aag cag gaa tgg agt cct agt cca ccc
                                                                     505
Ser Gly Ala Met Gly Pro Glu Lys Gln Glu Trp Ser Pro Ser Pro Pro
                           40
gcc acc cct gag cag ggc ctg tct gct ttc tac ctc tct tac ttt aac
                                                                     553
Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Tyr Leu Ser Tyr Phe Asn
                                                                     601
atg tat ccc gac gat agc tgg gtc gcc aaa gtc ccc gag gcc cgt
Met Tyr Pro Asp Asp Ser Ser Trp Val Ala Lys Val Pro Glu Ala Arg
                                       75
                                                                     649
qcc qqq gag gac cac ccg gag gag ccc gag cag tgt ccc gtc att gac
Ala Gly Glu Asp His Pro Glu Glu Pro Glu Gln Cys Pro Val Ile Asp
                                    90
                8.5
                                                                     697
age cag gee tet ggg age aeg ttg gat gag cae teg eta gag eag gtg
Ser Gln Ala Ser Gly Ser Thr Leu Asp Glu His Ser Leu Glu Gln Val
            100
                                105
caa tcg atg gtt gtg ggc gag gtc ctg aaa gat att gag acg gcc tgc
                                                                     745
Gln Ser Met Val Val Gly Glu Val Leu Lys Asp Ile Glu Thr Ala Cys
                           120
                                                125
aag ctt gtg aac atc aca gca gac cct ggg gac tgg agc cct ggt aac
                                                                     793
Lys Leu Val Asn Ile Thr Ala Asp Pro Gly Asp Trp Ser Pro Gly Asn
    130
                        135
                                                                     841
qtq caq aaq tqq ctt tta tgg aca gaa cac cag tac cgg ctg cct cca
Val Gln Lys Trp Leu Leu Trp Thr Glu His Gln Tyr Arg Leu Pro Pro
                                        155
                    150
gca ggc aag gcc ttc cag gag ctg ggc ggt aag gag ctg tgc gcc atg
                                                                     889
Ala Gly Lys Ala Phe Gln Glu Leu Gly Gly Lys Glu Leu Cys Ala Met
                                    170
                165
                                                                     937
tcc gag gaa cag ttc cgt cag cgt gca ccc ttg ggt ggg gat gta ctg
Ser Glu Glu Gln Phe Arg Gln Arg Ala Pro Leu Gly Gly Asp Val Leu
                                185
                                                    190
            180
cat gcc cac ctg gac atc tgg aag tca gcg gcc tgg atg aag gag agg
                                                                     985
His Ala His Leu Asp Ile Trp Lys Ser Ala Ala Trp Met Lys Glu Arg
                            200
ace teg cet ggg ace ett cae tae tge gee tee ace age gag gae gge
                                                                    1033 .
Thr Ser Pro Gly Thr Leu His Tyr Cys Ala Ser Thr Ser Glu Asp Gly
                                            220
    210
                        215
tgg acg gat ggt gag gtg gac tcg tgc tcc ggg cag ccc att cac
                                                                    1081
Trp Thr Asp Gly Glu Val Asp Ser Ser Cys Ser Gly Gln Pro Ile His
                    230
                                        235
ctg tgg cag ttc ctg aaa gaa ctg ctg ctc aag ccc cac agc tat ggc
                                                                    1129
Leu Trp Gln Phe Leu Lys Glu Leu Leu Lys Pro His Ser Tyr Gly
                                    250
                                                        255
```

```
cgc ttc atc cgg tgg ggt gtg cgc aag aac cgg cca gcc atg aac tat
                                                                     1177
Arg Phe Ile Arg Trp Gly Val Arg Lys Asn Arg Pro Ala Met Asn Tyr
                                265
            260
gat aaa cta aga agc tcc atc cgc tgg ctc aac aag gag aaa ggc atc
                                                                     1225
Asp Lys Leu Arg Ser Ser Ile Arg Trp Leu Asn Lys Glu Lys Gly Ile
                            280
                                                 285
                                                                     1273
ttc aaa att gag gac tca gca cag gtg gcc cga ctc cag tat tac aag
Phe Lys Ile Glu Asp Ser Ala Gln Val Ala Arg Leu Gln Tyr Tyr Lys
                        295
    290
aag ggc atg att cgt aaa ccc gcc atc tct cag cgc ctt gtc tac caa
                                                                     1321
Lys Gly Met Ile Arg Lys Pro Ala Ile Ser Gln Arg Leu Val Tyr Gln
                                         315
                    310
305
                                                                     1376
ttt gtg cat cca gtc tgagagccac agagaccaga ggcctacaac ctgccccagg
Phe Val His Pro Val
                325
cagccactct ctggttggcc tggtcctctc tgctcactct gaattcaggg gctgctggta
                                                                     1436
toccagaaco caaggtocca gatagacago cactgatota cocatacaca tgagototot
                                                                     1496
                                                                     1556
gggtcataca caggccccag gaagatcgag ggagctagtt cagcacacag ggactggacc
aagtcagctc accggacagt gatgtcactg gtctctgctc ctgccacaat cctgtaccat
                                                                     1616
atctggcatg gtgctaagag atgtctgtac cctgcgttgg gaagccaggg gtgccctggg
                                                                     1676
                                                                     1704
gatggataat aaagacgtaa gataactg
<210>
<211>
       325
<212>
       PRT
<213>
       Mus sp.
Met Gly Ser Ala Ser Pro Gly Leu Ser Asn Val Ser Pro Gly Cys Leu
Leu Leu Phe Pro Asp Val Ala Pro Arg Thr Gly Thr Glu Lys Ala Ala
Ser Gly Ala Met Gly Pro Glu Lys Gln Glu Trp Ser Pro Ser Pro Pro
Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Tyr Leu Ser Tyr Phe Asn
Met Tyr Pro Asp Asp Ser Ser Trp Val Ala Lys Val Pro Glu Ala Arg
Ala Gly Glu Asp His Pro Glu Glu Pro Glu Gln Cys Pro Val Ile Asp
Ser Gln Ala Ser Gly Ser Thr Leu Asp Glu His Ser Leu Glu Gln Val
                                 1.05
Gln Ser Met Val Val Gly Glu Val Leu Lys Asp Ile Glu Thr Ala Cys
                                                 125
                             120
Lys Leu Val Asn Ile Thr Ala Asp Pro Gly Asp Trp Ser Pro Gly Asn
Val Gln Lys Trp Leu Leu Trp Thr Glu His Gln Tyr Arg Leu Pro Pro
                    150
Ala Gly Lys Ala Phe Gln Glu Leu Gly Gly Lys Glu Leu Cys Ala Met
                                     170
                165
```

Ser	Glu	Glu	Gln 180	Phe	Arg	Gl'n	Arg	Ala 185	Pro	Leu	Gly	Gly	Asp 190	Val	Leu	
His	Ala	His 195	Leu	Asp	Ile	Trp	Lys 200	Ser	Ala	Ala	Trp	Met 205	Lys	Glu	Arg	
Thr	Ser 210	Pro	Gly	Thr	Leu	His 215	Tyr	Cys	Ala	Ser	Thr 220	Ser	Glu	Asp	Gly	
Trp 225	Thr	Asp	Gly	Glu	Val 230	Asp	Ser	Ser	Cys	Ser 235	Gly	Gln	Pro	Ile	His 240	
Leu	Trp	Gln	Phe	Leu 245	Lys	Glu	Leu	Leu	Leu 250	Lys	Pro	His	Ser	Tyr 255	Gly	
Arg	Phe	Ile	Arg 260	Trp	Gly	Val	Arg	Lys 265	Asn	Arg	Pro	Ala	Met 270	Asn	Tyr	
Asp	Lys	Leu 275	Arg	Ser	Ser	Ile	Arg 280	Trp	Leu	Asn	Lys	Glu 285	Lys	Gly	Ile	
Phe	Lys 290	Ile	Glu	Asp	Ser	Ala 295	Gln	Val	Ala	Arg	Leu 300	Gln	Tyr	Tyr	Lys	
Lys 305	Gly	Met	Ile	Arg	Lys 310	Pro	Ala	Ile	Ser	Gln 315	Arg	Leu	Val	Tyr	Gln 320	
Phe	Val	His	Pro	Val 325												
<210> 5 <211> 10 <212> DNA <213> Homo		10	sapi	iens												
<400 agc)> { ggcat	ā Egg														10
			sapi	iens										`		
<400 gccr)> (ccat	s gg														10